



STIC Search Report

Biotech-Chem Library

File Copy
09/21/04, 4:39
updated

STIC Database Tracking Number: 140315

TO: David Lamberston
Location: rem/2b79/2c70
Art Unit: 1636
Tuesday, December 14, 2004

Case Serial Number: 09/864486

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

O'Bryen, Barbara

From: Lambertson, David
Sent: Monday, December 13, 2004 8:35 AM
To: O'Bryen, Barbara
Cc: Lambertson, David
Subject: Search Request

Search Request

Examiner's Name:	David Lambertson
Examiner #:	79514
Art Unit:	1636
Room #:	02B79 Remsen
Mailbox room#:	02C70 Remsen
Phone:	(571) 272-0771
Results Format:	paper

Serial #:09/864,486

Please Search:

Nucleic Acid and Protein databases for:

SEQ ID No: 1 and 2

Including:

1. Default Search.
2. Interference Search.

Thanks,
Dave.

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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 13, 2004, 16:30:37 ; Search time 63 Seconds

(without alignments)
4099.763 Million cell updates/sec

Title: US-09-864-486A-1

Perfect score: 599

Sequence: 1 gtaataagagttctctaagta.....catcttttgccttggaac 360

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Rgapop 6.0 , Rgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 4004546

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=A Geneseq 23Sep04 -OPMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database : A.Geneseq 23Sep04: *
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2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	110	18.6	58	6 ABR62697	ABR62697 Yeast GCN
C 2	110	18.6	281	2 AAW02621	AAW02621 Yeast GCN
C 3	110	18.6	281	5 AAU08093	AAU08093 Yeast GCN
C 4	110	18.6	281	5 ABG94229	ABG94229 Yeast GCN
C 5	110	18.6	281	5 ABG93091	ABG93091 S. cerevi
C 6	110	18.6	281	5 ABG80541	ABG80541 Yeast gen
C 7	110	18.6	281	7 ADB67084	ADB67084 General c
C 8	110	18.6	281	8 ADL99355	ADL99355 Nanostruc
C 9	109	18.4	323	5 ABG93326	ABG93326 C. albica
C 10	102	17.2	49	6 ABU09710	ABU09710 Saccharom

C 11	98	16.6	266	2 AAR91295	Aar91295 Drosophil
C 12	92	15.5	36	8 ADF94459	Adf94459 Structure
C 13	91	15.4	281	2 AAW13955	Aaw13955 LZ varian
C 14	90.5	15.3	36	3 AAY88676	Aay88676 Core poly
C 15	90.5	15.3	36	4 AAB77031	Abb77031 Core poly
C 16	90.5	15.3	36	4 ABB01499	Abb01499 Viral cor
C 17	90.5	15.3	36	4 ABB00035	Abb00035 Viral DP1
C 18	90.5	15.3	36	4 AAU12584	Aau12584 DP178-lik
C 19	90.5	15.3	36	5 ADE01519	Ade01519 Hybrid po
C 20	89	15.0	35	4 AAG66864	Agg66864 Leucine z
C 21	89	15.0	35	6 ABG75995	Abg75995 Leucine z
C 22	88	15.0	35	6 AAE32714	Aae32714 Dimerisat
C 23	88	14.9	281	2 AAW02622	Aaw02622 Yeast GCN
C 24	87	14.7	33	3 AAY88745	Aay88745 Core poly
C 25	87	14.7	33	4 AAB77100	Abb77100 Core poly
C 26	87	14.7	33	4 AAE07425	Aae07425 Yeast PDA
C 27	87	14.7	33	4 ABB01569	Abb01569 Viral cor
C 28	87	14.7	33	4 ABB00104	Abb00104 Viral DP1
C 29	87	14.7	33	4 AAU12653	Aau12653 DP178-lik
C 30	87	14.7	33	5 AAE15760	Aae15760 PDA-3Hb p
C 31	87	14.7	33	5 AAU76769	Aau76769 PDA-3Hb p
C 32	87	14.7	33	5 ABG75547	Abg75547 Optimised
C 33	87	14.7	33	5 ADE01589	Ade01589 Hybrid po
C 34	87	14.7	33	8 ADF94454	Adf94454 Structure
C 35	87	14.7	35	8 ADM46699	Adm46699 GNC4 leuc
C 36	87	14.7	36	2 AAW95616	Aaw95616 Humanized
C 37	87	14.7	36	2 AAW30633	Aaw30633 Recombina
C 38	87	14.7	36	4 AAB66778	Aab66778 Leucine z
C 39	87	14.7	36	8 ADF94457	Adf94457 Structure
C 40	87	14.7	43	8 ADQ28739	Adq28739 Linked 80
C 41	87	14.7	44	2 AAY06684	Aay06684 Sequence
C 42	87	14.7	44	8 ADO39716	Ado39716 Fab'2 ant
C 43	87	14.7	45	2 AAW40588	Aaw40588 Human Fab
C 44	87	14.7	45	2 AAW92434	Aaw92434 Plasmid p
C 45	87	14.7	45	2 AAY29455	Aay29455 GCN4 leuc

ALIGNMENTS

RESULT 1

ABR62697

ID ABR62697 standard; protein; 58 AA.

XX ABR62697;

XX 06-NOV-2003 (first entry)

XX Yeast GCN4 basic domain leucine zipper domain.

XX Yeast; GCN4; biliverdin reductase; enzyme; haem oxygenase-1;

XX antiasthmatic; antiinflammatory; antiulcer; vasotropic; hypertensive;

XX antibacterial; gene therapy; antisense therapy; leucine zipper.

XX Saccharomyces cerevisiae.

XX Key Location/Qualifiers

FT Domain 18..23

FT Domain /label= Basic

FT Domain 30..58

FT Misc-difference 30 /label= Leucine_zipper

FT Misc-difference 37 /note= "L1 residue of leucine zipper"

FT Misc-difference 44 /note= "L2 residue of leucine zipper"

FT Misc-difference 51 /note= "L3 residue of leucine zipper"

FT Misc-difference 58 /note= "L4 residue of leucine zipper"

FT Misc-difference 58 /note= "L5 residue of leucine zipper"

XX WO2003055981-A2.

XX

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1  RESULT 1
2  US-08-347-792-4
3  ; Sequence 4, Application US/08347792
4  ; Patent No. 5573925
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Halazonetis, Thanos D.
7  ; TITLE OF INVENTION: p53 Proteins With Altered
8  ; TITLE OF INVENTION: Tetramerization Domains
9  ; NUMBER OF SEQUENCES: 37
10 ; CORRESPONDENCE ADDRESS:
11 ; ADDRESSEE: Howson and Howson
12 ; STREET: Spring House Corporate Cntr., PO Box 457
13 ; CITY: Spring House
14 ; STATE: Pennsylvania
15 ; COUNTRY: USA
16 ; ZIP: 19477
17 ; COMPUTER READABLE FORM:
18 ; MEDIUM TYPE: Floppy disk
19 ; COMPUTER: IBM PC compatible
20 ; OPERATING SYSTEM: PC-DOS/MS-DOS
21 ; SOFTWARE: Patent In Release #1.0, Version #1.25
22 ; CURRENT APPLICATION DATA:
23 ; APPLICATION NUMBER: US/08/347,792
24 ; FILING DATE:
25 ; CLASSIFICATION: 530
26 ; ATTORNEY/AGENT INFORMATION:
27 ; NAME: Bak, Mary E.
28 ; REGISTRATION NUMBER: 31,215
29 ; REFERENCE/DOCKET NUMBER: WSP58USA
30 ; TELECOMMUNICATION INFORMATION:
31 ; TELEPHONE: 215-540-9206
32 ; TELEFAX: 215-540-5818
33 ; INFORMATION FOR SEQ ID NO: 4:
34 ; SEQUENCE CHARACTERISTICS:
35 ; LENGTH: 281 amino acids
36 ; TYPE: amino acid

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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 13, 2004, 18:14:18 ; Search time 55.8 Seconds
(without alignments)
4608.753 Million cell updates/sec

Title: US-09-864-486A-1
Perfect score: 599
Sequence: 1 gaataggagtctctaagta.....catcttctagcccttgaac 360

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 3171152

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
c 1	110	18.6	281	9	US-09-801-368-120	Sequence 120, App
c 2	110	18.6	281	10	US-09-848-616-154	Sequence 154, App
c 3	110	18.6	281	14	US-10-050-902-154	Sequence 154, App
c 4	110	18.6	281	14	US-10-050-898-154	Sequence 154, App
c 5	110	18.6	281	14	US-10-080-608A-15	Sequence 15, Appl
c 6	110	18.6	281	14	US-10-370-685-104	Sequence 104, App
c 7	110	18.6	281	16	US-10-451-467A-140	Sequence 140, App
c 8	109	18.4	323	16	US-10-451-467A-610	Sequence 610, App
c 9	102	17.2	49	15	US-10-622-064-12	Sequence 12, Appl
c 10	92	15.5	36	14	US-10-283-403-6	Sequence 6, Appl
c 11	90.5	15.3	36	14	US-10-351-641-26	Sequence 26, Appl
c 12	89	15.0	35	13	US-10-057-505-17	Sequence 17, Appl
c 13	87	14.7	33	14	US-10-351-641-96	Sequence 96, Appl
c 14	87	14.7	33	14	US-10-283-403-1	Sequence 1, Appl
c 15	87	14.7	33	17	US-10-851-564-4	Sequence 4, Appl
c 16	87	14.7	36	9	US-09-940-166A-3	Sequence 3, Appl
c 17	87	14.7	36	14	US-10-283-403-4	Sequence 4, Appl
c 18	87	14.7	36	16	US-10-762-967-3	Sequence 3, Appl
c 19	87	14.7	43	14	US-10-347-960-26	Sequence 26, Appl
c 20	87	14.7	45	10	US-09-726-258-57	Sequence 57, Appl
c 21	87	14.7	48	14	US-10-247-960-29	Sequence 29, Appl
c 22	87	14.7	55	14	US-10-247-960-5	Sequence 5, Appl
c 23	87	14.7	55	17	US-10-730-776-14	Sequence 14, Appl
c 24	87	14.7	60	14	US-10-247-960-6	Sequence 6, Appl
c 25	87	14.7	60	17	US-10-730-776-15	Sequence 15, Appl
c 26	87	14.7	298	10	US-09-726-258-60	Sequence 60, Appl
c 27	87	14.7	300	9	US-09-940-166A-7	Sequence 7, Appl
c 28	87	14.7	300	14	US-10-227-694-2	Sequence 2, Appl
c 29	87	14.7	300	16	US-10-762-967-7	Sequence 7, Appl
c 30	83	14.0	52	15	US-10-344-620-2	Sequence 2, Appl
c 31	83	14.0	191	15	US-10-344-620-6	Sequence 6, Appl
c 32	82	13.9	32	10	US-09-259-658-5	Sequence 5, Appl
c 33	82	13.9	32	10	US-09-491-614-4	Sequence 4, Appl
c 34	82	13.9	32	14	US-10-103-597A-4	Sequence 4, Appl
c 35	82	13.9	32	14	US-10-161-205-3	Sequence 3, Appl
c 36	82	13.9	32	14	US-10-101-001-3	Sequence 3, Appl
c 37	82	13.9	32	14	US-10-188-444-4	Sequence 4, Appl
c 38	82	13.9	33	9	US-09-796-202-6	Sequence 6, Appl
c 39	82	13.9	33	14	US-10-032-314-316	Sequence 316, App
c 40	82	13.9	33	14	US-10-323-314-6	Sequence 6, Appl
c 41	82	13.9	298	14	US-10-273-180-4	Sequence 4, Appl
c 42	81	13.7	33	14	US-10-338-083-18	Sequence 18, Appl
c 43	81	13.7	33	16	US-10-611-399-18	Sequence 18, Appl
c 44	81	13.7	36	14	US-10-283-403-8	Sequence 8, Appl
c 45	81	13.7	52	15	US-10-395-817-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-801-368-120
; Sequence 120, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07

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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 13, 2004, 17:56:18 : Search time 18 Seconds
(without alignments)
3848.671 Million cell updates/sec

Title: US-09-864-486A-1

Perfect score: 599

Sequence: 1 gtaataggagtctctaagta.....catcttcttagccctggaac 360

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=500 -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptp -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
C	1	110	18.6	281	1	amino acid biosynt
C	2	89	15.0	2201	1	genome polyprotein
C	3	81	13.7	2185	1	genome polyprotein
C	4	81	13.7	2185	1	genome polyprotein
C	5	75	12.7	1091	2	diaphanous protein
C	6	70	11.8	582	2	bps2 protein - Des
C	7	69.5	11.7	2206	1	genome polyprotein
C	8	69.5	11.7	2206	1	genome polyprotein
C	9	68.5	11.6	2207	1	genome polyprotein
C	10	68.5	11.6	2209	1	genome polyprotein
C	11	68.5	11.6	2209	1	genome polyprotein
C	12	68.5	11.6	2209	1	genome polyprotein
C	13	67.5	11.3	401	2	probable aminotran
C	14	67	11.3	2214	1	genome polyprotein

15	66	11.0	83	2	AE1913	hypothetical prote
16	66	11.0	664	2	C84747	probable protein k
C 17	66	11.1	1379	2	KRSHL1	protoporphyrin IX
C 18	65	11.0	412	1	A61404	keratin, 48K type
C 19	65	11.0	416	2	S60034	keratin A, type I
C 20	65	11.0	416	2	S60034	keratin H, type I
C 21	65	11.0	416	2	A46559	keratin, type I, h
C 22	65	10.9	628	2	T05900	phosphoenolpyruvat
C 23	65	10.9	2405	2	T08164	dynein alpha heavy
C 24	64.5	10.9	1140	1	S38908	UV-damaged DNA-bin
C 25	64.5	10.9	1140	1	S38908	UV-damaged DNA-bin
C 26	64.5	10.9	1140	2	JC7152	UV-damaged DNA-bin
C 27	64	10.8	354	2	T06487	probable DNA-bind
C 28	64	10.7	355	2	F96940	beta-mannanase (im
C 29	64	10.8	357	2	S50821	DNA-binding protei
C 30	64	10.8	593	2	A71532	probable phosphoma
C 31	64	10.7	670	2	S52637	phosphoenolpyruvat
C 32	64	10.8	2182	1	GNNYB1	genome polyprotein
C 33	63.5	10.6	144	2	G69425	hypothetical prote
C 34	63.5	10.7	547	2	F69964	amino acid degrada
C 35	63.5	10.6	714	2	S66699	hypothetical prote
C 36	63	10.6	190	2	B72416	conserved hypothet
C 37	63	10.6	296	1	TVFVJN	transforming prote
C 38	63	10.6	327	2	F71980	hypothetical prote
C 39	63	10.6	392	2	A60777	keratin 2, type I,
C 40	63	10.6	404	2	JS0073	keratin, 47.6k typ
C 41	63	10.6	405	2	T45615	hypothetical prote
C 42	62.5	10.6	269	1	A30208	cross-pathway cont
C 43	62.5	10.4	280	2	T28225	ORF MSV064 hypothe
C 44	62.5	10.6	329	2	F86675	mevalonate kinase
C 45	62.5	10.4	739	2	A46159	interferon-depende

ALIGNMENTS

RESULT 1

RGBYA2

amino acid biosynthesis regulatory protein - yeast (Saccharomycetes cerevisiae)
N;Alternate names: protein YEL009C
C;Species: Saccharomycetes cerevisiae
C;Date: 27-Nov-1985 #sequence revision 27-Nov-1985 #text_change 09-Jul-2004
C;Accession: A03605; S50450; A03604
R;Hinnebusch, A.G.
Proc. Natl. Acad. Sci. U.S.A. 81, 6442-6446, 1984
A;Title: Evidence for translational regulation of the activator of general amino acid
A;Reference number: A03605; PMID:85038531; PMID:6387704
A;Accession: A03605
A;Molecule type: DNA
A;Residues: 1-281 <HIN>
A;Cross-references: UNIPROT:P03069; EMBL:K02205; NID:gl71581; PIDN:AAA34640.1; PID:gl7
R;Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A;Description: Saccharomycetes cerevisiae chromosome V cosmids 9871, 8199, 9867, 9495 an
A;Reference number: S50428
A;Accession: S50450
A;Molecule type: DNA
A;Residues: 1-281 <DIE>
A;Cross-references: EMBL:U18530; NID:g602367; PIDN:AAB64486.1; PID:g602376; GSPDB:GN00
R;Thiross, G.; Penn, M.D.; Greer, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 5096-5100, 1984
A;Title: 5' untranslated sequences are required for the translational control of a yeast
A;Reference number: A03604; PMID:84298088; PMID:6433345
A;Accession: A03604
A;Molecule type: DNA
A;Residues: 1-238, 'PGVLVRESCKE' <THI>
A;Cross-references: EMBL:K02649; NID:gl71585; PIDN:AAA65521.1; PID:gl71586
C;Genetics:
A;Gene: SGD:GCN4; MIPS:YEL009C
A;Cross-references: SGD:S0000735; MIPS:YEL009C
C;Function:
A;Description: transcription regulation
A;Note: required under amino acid starvation conditions for increasing the transcripti

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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 13, 2004, 16:32:22 ; Search time 81.9 Seconds
(without alignments)

5058.239 Million cell updates/sec

Title: US-09-864-486A-1

Perfect score: 599

Sequence: 1 gtaattaggagttcttaagta.....catctttctagccttggaac 360

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US09864486/runat.13122004.100259.1961/app.query.fasta_1.910
-DB=uniprot_02 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09864486 @CGN 1.1.141 @runat.13122004.100259.1961 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	119	20.1	281	Q6C4D2	O6C4D2 yarrowia li
C 2	118	19.9	325	Q75AC9	Q75AC9 ashbya goss
C 3	118	19.9	325	AAS51909	AAS51909 ashbya go
C 4	112	18.9	314	Q877C4	Q877C4 candida mal
C 5	112	18.9	333	Q6CQU7	Q6CQU7 kluyveromyc
C 6	110	18.6	281	1 GCN4 YEAST	P03069 saccharomyc
C 7	110	18.6	281	Q70D88	Q70D88 saccharomyc
C 8	110	18.6	281	Q70D91	Q70D91 saccharomyc
C 9	110	18.6	281	Q70D96	Q70D96 saccharomyc
C 10	110	18.6	281	Q70D99	Q70D99 saccharomyc
C 11	110	18.6	281	Q70DA0	Q70DA0 saccharomyc
C 12	110	18.6	281	CAE52206	CAE52206 saccharomyc
C 13	110	18.6	281	CAE52207	CAE52207 saccharomyc
C 14	110	18.6	281	CAE52208	CAE52208 saccharomyc
C 15	110	18.6	281	CAE52209	CAE52209 saccharomyc
C 16	110	18.6	281	CAE52210	CAE52210 saccharomyc

C 17	110	18.6	281	2	CAE52211	saccharom
C 18	110	18.6	281	2	CAE52212	saccharom
C 19	110	18.6	281	2	CAE52213	saccharom
C 20	110	18.6	281	2	CAE52214	saccharom
C 21	110	18.6	281	2	CAE52215	saccharom
C 22	110	18.6	281	2	CAE52216	saccharom
C 23	110	18.6	281	2	CAE52217	saccharom
C 24	110	18.6	281	2	CAE52218	saccharom
C 25	110	18.6	281	2	CAE52219	saccharom
C 26	110	18.6	281	2	CAE52220	saccharom
C 27	110	18.6	281	2	CAE52221	saccharom
C 28	110	18.6	281	2	CAE52222	saccharom
C 29	110	18.6	281	2	CAE52223	saccharom
C 30	110	18.6	281	2	CAE52224	saccharom
C 31	109	18.4	322	2	Q9UV12	O9UV12 candida alb
C 32	106	17.9	310	2	Q6FL16	O6FL16 candida gla
C 33	94	15.9	287	2	Q6BW79	Q6BW79 debaryomyce
C 34	89	15.0	118	2	Q6VD37	Q6VD37 human coxa
C 35	89	15.0	118	2	Q6VD43	Q6VD43 human coxa
C 36	89	15.0	118	2	Q6VD45	Q6VD45 human coxa
C 37	89	15.0	118	2	Q6VD83	Q6VD83 human coxa
C 38	89	15.0	118	2	Q6VD84	Q6VD84 human coxa
C 39	89	15.0	118	2	Q6VD85	Q6VD85 human coxa
C 40	89	15.0	118	2	Q6VD86	Q6VD86 human coxa
C 41	89	15.0	118	2	Q6VDG7	Q6VDG7 human coxa
C 42	89	15.0	118	2	Q6VDG8	Q6VDG8 human coxa
C 43	89	15.0	118	2	Q6VDK6	Q6VDK6 human coxa
C 44	89	15.0	118	2	Q6VDL0	Q6VDL0 human coxa
C 45	89	15.0	118	2	AAQ95293	AAQ95293 human cox

ALIGNMENTS

RESULT 1
Q6C4D2 PRELIMINARY; PRT; 281 AA.
ID Q6C4D2
AC Q6C4D2
DT 01-OCT-2004 (TREMBLrel. 28, Created)
DT 01-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Chromosome E of strain CLIB99 of Yarrowia lipolytica.
GN ORFNames=YALI0E277429;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG GENOLEVURES;
RA Lafontaine I., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Dujon B., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Boismare A., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Despons L., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Hantraye F., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicoud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG GENOSCOPE;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR382131; CAG80083.1;
SQ SEQUENCE 281 AA; 30378 MW; 16BF8B2D3AF86C96 CRC64;

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2004, 14:03:27 ; Search time 2078.4 Seconds
(without alignments)
8191.056 Million cell updates/sec

Title: US-09-864-486A-1
Perfect score: 360
Sequence: 1 gtaataggagttcttaagta.....catcttcttagccctggaac 360

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_scs.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	360	100.0	360	BD175189	BD175189 DNA fragm
2	360	100.0	360	AX323247	AX323247 Sequence
3	360	100.0	2696	PPA272040	AX272040 Pichia pa
C 4	62.8	17.4	1824	AR064394	AR064394 Sequence
C 5	62.8	17.4	1824	I28708	I28708 Sequence 3
C 6	62.8	17.4	1824	I89362	I89362 Sequence 3
C 7	62.8	17.4	1824	YSCGCN4	K02205 Yeast (S.c
C 8	62.8	17.4	2089	YSCGCN4B	K02649 Yeast (S.c
C 9	62.8	17.4	62643	SCE9871	U18530 Saccharomyc
C 10	62.8	17.4	110000	2 AC141230_2	Continuation (3 of
C 11	54	15.0	1580	AF205716	AF205716 Candida a
C 12	53.4	14.8	972	AX537008	AX537008 Sequence
C 13	53	14.7	846	AJ585686	AJ585686 Saccharom
C 14	53	14.7	846	AJ585687	AJ585687 Saccharom
C 15	53	14.7	846	AJ585688	AJ585688 Saccharom
C 16	53	14.7	846	AJ585689	AJ585689 Saccharom
C 17	53	14.7	846	AJ585690	AJ585690 Saccharom
C 18	53	14.7	846	AJ585691	AJ585691 Saccharom
C 19	53	14.7	846	AJ585692	AJ585692 Saccharom

C 20	53	14.7	846	8	AJ585693	Saccharom
C 21	53	14.7	846	8	AJ585694	Saccharom
C 22	53	14.7	846	8	AJ585695	Saccharom
C 23	53	14.7	846	8	AJ585696	Saccharom
C 24	53	14.7	846	8	AJ585697	Saccharom
C 25	53	14.7	846	8	AJ585698	Saccharom
C 26	53	14.7	846	8	AJ585699	Saccharom
C 27	53	14.7	846	8	AJ585700	Saccharom
C 28	53	14.7	846	8	AJ585701	Saccharom
C 29	53	14.7	846	8	AJ585702	Saccharom
C 30	53	14.7	846	8	AJ585703	Saccharom
C 31	53	14.7	846	8	AJ585704	Saccharom
C 32	53	14.7	1346	6	AX336538	Sequence
C 33	52.2	14.5	2800	8	AB063247	AB063247 Candida m
C 34	51.6	14.3	110000	8	CR380958_02	Continuation (3 of
C 35	47.4	13.2	110000	8	CR382134_10	Continuation (11 o
C 36	47	13.1	7104	6	AX281477	AX281477 Sequence
C 37	47	13.1	7104	6	AX348827	AX348827 Sequence
C 38	45.2	12.6	95202	10	AL928807	AL928807 Mouse DNA
C 39	44.8	12.4	110000	8	CR382124_12	Continuation (13 o
C 40	44.2	12.3	798	6	AR473525	AR473525 Sequence
C 41	44.2	12.3	110000	8	CR382131_32	Continuation (33 o
C 42	44.2	12.3	132728	2	AC099411	AC099411 Felis cat
C 43	44.2	12.3	220251	2	AC150374	AC150374 Colobus g
C 44	43.2	12.0	6763	6	AX251241	AX251241 Sequence
C 45	43.2	12.0	6763	6	AX281459	AX281459 Sequence

ALIGNMENTS

RESULT 1
BD175189
LOCUS DNA fragment of a mechiru nutrition nature picha pathtorisu yeast
DEFINITION ICL gene.
ACCESSION BD175189
VERSION BD175189.1 GI:29120883
KEYWORDS JP 2002253235-A/2.
SOURCE Pichia pastoris
ORGANISM Pichia pastoris
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.
REFERENCE 1 (bases 1 to 360)
AUTHORS Dias,J.M., Prado,I.V. and Leon,N.C.
TITLE DNA fragment of a mechiru nutrition nature picha pathtorisu yeast
JOURNAL ICL gene
Patent: JP 2002253235-A 2 10-SEP-2002;
CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA
OS Pichia pastoris (Yeast)
PN JP 2002253235-A/2
PD 10-SEP-2002
PF 28-MAY-2001 JP 2001159321
PR 26-MAY-2000 CU 2000-122
PI JAVIER MENENDEZ DIAS,IRIS VALDEZ PRADO,NELSON CABRERA LEON PC
C12N15/09,C12N15/00
CC Secuencia que contiene la region 3' no codificante del gen CC
FH Key ICL.
FT terminator Location/Qualifiers
Location/Qualifiers
1..360
/organism="Pichia pastoris"
/mol_type="genomic DNA"
/db_xref="taxon:4922"
ORIGIN
Query Match 100.0%; Score 360; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.3e-76;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTAATAGAGTCTCCTAGTAAAGTAATAATTGACTTGAGGTATTATAGATTGTGTGT 60
|||||

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2004, 14:02:37 ; Search time 339 Seconds

(without alignments)
5574.606 Million cell updates/sec

Title: US-09-864-486A-1
Perfect score: 360

Sequence: 1 gtaataggagttcctaagta.....catcttcttagccctggaac 360

Scoring table: IDENTITY NUC
Gap0 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001ae:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	358.4	99.6	360	ABK13231	Abk13231 P. pastor
2	62.8	17.4	1824	AAT32832	Aat32832 Yeast GCN
3	53.4	14.8	972	ABQ76592	Abq76592 C. albica
4	53	14.7	1346	ABQ76357	Abq76357 S. cerevi
5	52.2	14.5	2684	ADP57624	Adp57624 Yeast GCN
6	47	13.1	7104	ABL34588	AbL34588 Human met
7	47	13.1	7104	ABL70395	AbL70395 Chemicall
8	44.2	12.3	798	AAT14025	Aat14025 Drosophil
9	43.2	12.0	6763	AAS46487	Aas46487 Tumour su
10	43.2	12.0	6763	ABL33554	AbL33554 Human imm
11	43.2	12.0	6763	ABL34570	AbL34570 Human met
12	43.2	12.0	6763	ABN80196	Abn80196 Human che
13	43	11.9	175	AAL46025	Aal46025 Peptide d
14	43	11.9	175	AAL46026	Aal46026 pGADDA24
15	43	11.9	586	AAL46021	Aal46021 NLS and t
16	42	11.7	156	AAL46020	Aal46020 DNA bindi
17	41.8	11.6	8771	ABL33825	AbL33825 Human imm
18	41.6	11.6	12763	ABL32302	AbL32302 Human imm
19	41.4	11.5	504	ABQ73929	Abq73929 Chimeric
20	41.4	11.5	525	ABQ73935	Abq73935 TBD-ci-bz
21	41.4	11.5	542	ABQ73934	Abq73934 TBD-ci-bz

C 22	41.2	11.4	5020	8	ABZ10105	Abz10105 Haematopo
C 23	40.8	11.3	8718	6	ABL33273	AbL33273 Human imm
C 24	40.4	11.2	6196	6	ABL33864	AbL33864 Human imm
C 25	40.2	11.2	606	5	ABV49913	Abv49913 Human pro
C 26	40	11.1	897	12	ADI23637	Adi23637 Yeast GCN
C 27	40	11.1	5489	6	ABL34120	AbL34120 Human imm
C 28	39.4	10.9	10133	6	ABL32458	AbL32458 Human imm
C 29	39.2	10.9	966	6	ABL87946	AbL87946 DNA polym
C 30	39.2	10.9	966	6	ABL87945	AbL87945 DNA polym
C 31	38.8	10.8	6912	6	ABK28371	AbK28371 DNA trans
C 32	38.6	10.7	16633	6	ABN79984	Abn79984 Human che
C 33	38.6	10.7	18434	6	ABL34007	AbL34007 Human imm
C 34	38.6	10.7	58155	6	ABN87364	Abn87364 Human lip
C 35	38.4	10.7	6316	4	AAS46351	Aas46351 Tumour su
C 36	38.4	10.7	6316	6	ABK31260	AbK31260 Signal tr
C 37	38.4	10.7	6316	6	ABL70215	AbL70215 Chemicall
C 38	38.4	10.7	6321	6	AAS61170	Aas61170 Human gen
C 39	38.4	10.7	6321	6	ABQ67063	AbQ67063 Human ang
C 40	38.2	10.6	9770	6	ABL32032	AbL32032 Human imm
C 41	38.2	10.6	83391	6	ABQ67093	AbQ67093 Human ang
C 42	38	10.6	4993	6	ABL34103	AbL34103 Human imm
C 43	38	10.6	5020	8	ABZ09959	Abz09959 Haematopo
C 44	38	10.6	5234	6	ABL32945	AbL32945 Human imm
C 45	38	10.6	6250	6	ABN80215	Abn80215 Human che

ALIGNMENTS

RESULT 1

ABK13231
ID ABK13231 standard; DNA; 360 BP.

AC ABK13231;

DT 23-APR-2002 (first entry)

DE P. pastoris isocitrate lyase gene 3' UTR.

KW Isocitrate lyase; ICL; 3' UTR; ds; yeast, heterologous gene expression.

OS Pichia pastoris.

PN EP1162266-A2.

PD 12-DEC-2001.

PF 28-MAY-2001; 2001EP-00202009.

PR 26-MAY-2000; 2000CU-00000122.

PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.

PI Menendez Diaz J, Valdes Prado I, Cabrera Leon N;

DR WPI; 2002-084415/12.

PT New recombinant DNA fragment for protein production, contains an isocitrate lyase encoding gene from Pichia pastoris, which regulates heterologous gene expression in yeasts, when operably linked to the fragment.

PS Claim 1; Page 8; 18pp; English.

XX The invention relates to a recombinant DNA fragment (I) comprising a sequence (S) of 684bp (the 5' region of the Pichia pastoris isocitrate lyase, ICL, gene including the promoter) or 360bp (the 3' UTR including a terminator), given in the specification, where (I) belongs to an isocitrate lyase encoding gene (ICL) from Pichia pastoris, which is able to regulate heterologous gene expression in yeasts, when it is operably linked to (I), and including regulatory elements necessary for heterologous gene expression. The DNA fragment is useful for expressing heterologous proteins in Pichia pastoris, for expressing a foreign gene,

Result No.	Score	Query		DB	ID	Description
		Match	Length			
C 1	62.8	17.4	1824	1	US-08-347-792-3	Sequence 3, Appli
C 2	62.8	17.4	1824	1	US-08-431-357-3	Sequence 3, Appli
C 3	62.8	17.4	1824	2	US-08-697-221-5	Sequence 5, Appli
C 4	62.8	17.4	1824	5	PCR-US95-15353-3	Sequence 3, Appli
C 5	52	14.4	945	4	US-09-248-796A-4712	Sequence 4712, Ap
C 6	44.2	12.3	798	2	US-08-319-866-7	Sequence 7, Appli
C 7	44.2	12.3	798	4	US-08-909-917-7	Sequence 7, Appli
C 8	37.2	10.3	1824	1	US-08-347-792-5	Sequence 5, Appli
C 9	37.2	10.3	1824	1	US-08-431-357-5	Sequence 5, Appli
C 10	37.2	10.3	1824	5	PCR-US95-15353-5	Sequence 5, Appli
C 11	37.2	10.3	2523	4	US-09-620-312D-290	Sequence 290, App
C 12	36	10.0	525	4	US-08-956-171E-539	Sequence 539, App
C 13	36	10.0	525	4	US-08-781-986A-539	Sequence 539, App
C 14	36	10.0	9319	3	US-08-880-179-1	Sequence 1, Appli
C 15	35.8	9.9	10144	4	US-10-204-708-94	Sequence 94, Appl
C 16	35.4	9.8	5666	4	US-10-204-708-29	Sequence 29, Appl
C 17	35.2	9.8	399	4	US-09-621-976-8976	Sequence 8976, Ap
C 18	35.2	9.8	3300	2	US-08-913-843-4	Sequence 4, Appli
C 19	34.8	9.7	151	2	US-08-256-790-3	Sequence 3, Appli
C 20	34.8	9.7	1141	4	US-09-806-708B-22	Sequence 22, Appl
C 21	34.8	9.7	7664	4	US-10-204-708-83	Sequence 83, Appl
C 22	34.8	9.7	10467	4	US-10-204-708-1	Sequence 1, Appli
C 23	34.4	9.6	8961	4	US-10-204-708-79	Sequence 79, Appl
C 24	34.2	9.5	1064	3	US-09-149-922-3	Sequence 3, Appli
C 25	33.8	9.4	1055	4	US-09-806-708B-23	Sequence 23, Appl
C 26	33.8	9.4	6583	4	US-10-204-708-26	Sequence 26, Appl
C 27	33.6	9.3	5152	4	US-10-204-708-48	Sequence 48, Appl

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2004, 15:27:22 ; Search time 354 Seconds
(without alignments)
5606.970 Million cell updates/sec

Title: US-09-864-486A-1
Perfect score: 360
Sequence: 1 gtaataggaggtcctaagta.....catcttttagcccttgaac 360

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4085731 seqs, 2756760397 residues

Total number of hits satisfying chosen parameters: 8171462

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	360	100.0	360	11	US-09-864-486A-1
2	240	66.7	240	11	US-09-864-486A-2
3	53.4	14.8	972	17	US-10-451-467A-609
4	53	14.7	846	9	US-09-801-368-119
5	53	14.7	1346	17	US-10-451-467A-139
6	47	13.1	7104	15	US-10-240-485-141
7	43.2	12.0	6763	15	US-10-311-455-1527
8	43.2	12.0	6763	15	US-10-240-485-123
9	43.2	12.0	6763	16	US-10-221-714A-209
10	43	11.9	175	16	US-10-344-620-10
11	43	11.9	175	16	US-10-344-620-11
12	43	11.9	586	16	US-10-344-620-5

C 13	42	11.7	156	16	US-10-344-620-4
C 14	41.8	11.6	8771	15	US-10-311-455-1798
C 15	41.6	11.6	12763	15	US-10-311-455-275
C 16	41.4	11.5	504	14	US-10-032-827A-12
C 17	41.4	11.5	525	14	US-10-032-827A-18
C 18	41.4	11.5	542	14	US-10-032-827A-17
C 19	41.2	11.4	5020	18	US-10-473-126-245
C 20	40.8	11.3	8718	15	US-10-473-126-245
C 21	40.4	11.2	6196	15	US-10-311-455-1837
C 22	40	11.1	897	15	US-10-273-180-3
C 23	40	11.1	5489	15	US-10-311-455-2093
C 24	39.4	10.9	10133	15	US-10-311-455-431
C 25	39.4	10.9	3673778	15	US-10-312-841-2
C 26	38.2	10.9	966	10	US-09-906-179A-16
C 27	39.2	10.9	966	10	US-09-906-179A-17
C 28	38.8	10.8	288	18	US-10-425-115-3622
C 29	38.8	10.8	6912	15	US-10-240-453-245
C 30	38.6	10.7	388	17	US-10-437-963-1934
C 31	38.6	10.7	18434	15	US-10-311-455-1980
C 32	38.6	10.7	53155	9	US-09-735-933-3
C 33	38.4	10.7	6316	16	US-10-221-613-129
C 34	38.4	10.7	6316	16	US-10-221-714A-73
C 35	38.4	10.7	6321	17	US-10-433-793-93
C 36	38.2	10.6	9770	15	US-10-311-455-5
C 37	38.2	10.6	83391	17	US-10-433-793-123
C 38	38	10.6	689	13	US-10-027-632-185044
C 39	38	10.6	689	15	US-10-027-632-185044
C 40	38	10.6	4993	15	US-10-311-455-2076
C 41	38	10.6	5020	18	US-10-473-126-99
C 42	38	10.6	5234	15	US-10-311-455-918
C 43	38	10.6	7591	15	US-10-074-024-841
C 44	37.8	10.5	6123	15	US-10-311-455-794
C 45	37.8	10.5	3673778	15	US-10-312-841-1

ALIGNMENTS

RESULT 1

US-09-864-486A-1

; Sequence 1, Application US/09864486A

; Publication No. US20040106783A1

; GENERAL INFORMATION:

; APPLICANT: Menendez Diaz, Javier

; APPLICANT: Valdes Prado, Chris

; APPLICANT: Cabrera Leon, Nelson

; TITLE OF INVENTION: DNA Fragments of the Methylotrophic Pichia Pastoris Yeast iCL 9

; FILE REFERENCE: 976-9

; CURRENT APPLICATION NUMBER: US/09/864,486A

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 360

; TYPE: DNA

; ORGANISM: Pichia pastoris

US-09-864-486A-1

Query Match	100.0%;	Score 360;	DB 11;	Length 360;
Best Local Similarity	100.0%;	Pred. No. 4.5e-83;		
Matches 360;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GTAATAGGAGTTCCTAAGTAGTAAAGATAATGACTTGAGGTATTTATAGATTGTGTGT	60	
Db	1	GTAATAGGAGTTCCTAAGTAGTAAAGATAATGACTTGAGGTATTTATAGATTGTGTGT	60	
Qy	61	AGGTAATATCTATGTCGTCCATCTTACCTTGGTGGGTGACGGGGCGGTGAATAATC	120	
Db	61	AGGTAATATCTATGTCGTCCATCTTACCTTGGTGGGTGACGGGGCGGTGAATAATC	120	
Qy	121	AGTTCGGATCAAGACTTTTACACCTTGTCCACAGAGGGTCCGCTCTACTGATTACTACA	180	
Db	121	AGTTCGGATCAAGACTTTTACACCTTGTCCACAGAGGGTCCGCTCTACTGATTACTACA	180	

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2004, 14:10:32 ; Search time 2267.4 Seconds
(without alignments)
5785.615 Million cell updates/sec

Title: US-09-864-486A-1
Perfect score: 360
Sequence: 1 gtaataggattcctaagta.....catcttttagccctggaac 360

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_est4.*
- 5: gb_est5.*
- 6: gb_est6.*
- 7: gb_est7.*
- 8: gb_est8.*
- 9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61.4	17.1	323	7 T36997	T36997 EST102040 S
2	61.4	17.1	363	7 T36351	T36351 EST101276 S
3	61	16.9	263	7 T37110	T37110 EST102177 S
4	60.8	16.9	370	7 T36326	T36326 EST101246 S
5	59.8	16.6	320	7 T38676	T38676 EST104204 S
6	57	15.8	210	7 T38672	T38672 EST104198 S
7	48.8	13.6	987	9 CNS06PHH	AL409371 T3 end of
8	46	12.8	476	1 AI399548	AI399548 NCSP6C2T7
9	44.8	12.4	440	2 AW870991	AW870991 ra53402.Y
10	44.8	12.4	542	2 AW827656	AW827656 ra45607.Y
11	44.4	12.3	904	9 CNS06NCH	AL406599 T3 end of
12	43.8	12.2	430	1 AU267015	AU267015 AU267015
13	43.8	12.2	459	6 C93400	C93400 C93400 Dict
14	43.8	12.2	487	1 AU267016	AU267016 AU267016
15	43.4	12.1	611	9 CE651766	CE651766 tigr-gss-
16	42.2	11.7	957	9 CL054187	CL054187 CH216-78N
17	42	11.7	438	8 BZ286848	BZ286848 SALK_0201
18	41.8	11.6	605	6 CF308474	CF308474 ABF--02-F
19	41.8	11.6	870	9 CNS06UZZ	AL416517 T7 end of
20	41.6	11.6	297	9 CNS03NEJ	AL251956 Tetradon
21	41.2	11.4	388	8 BZ382828	BZ382828 SALK_1189
22	41.2	11.4	610	2 BB770903	BB770903 BB770903
23	40.8	11.3	1101	9 CNS00LSY	AL068053 Drosophila
24	40.8	11.3	1101	9 CNS00ZB7	AL097453 Drosophila

25	40.4	11.2	306	8 AQ965507	AQ965507 LERIC73TR
26	40.2	11.2	307	9 CNS032BQ	AL224639 Tetradon
27	40.2	11.2	989	9 CNS015P2	AL105761 Drosophila
28	40	11.1	798	8 BH493781	BH493781 BOHAK82TF
29	39.8	11.1	329	6 CF329701	CF329701 NACL--OS-
30	39.8	11.1	744	9 CNS01117	AL100297 Drosophila
31	39.8	11.1	829	7 COS56235	CO56235 AGENCOURT
32	39.4	10.9	413	8 BH502230	BH502230 BOGT242TF
33	39.4	10.9	727	9 CNS00ZOR	AL097077 Drosophila
34	39.4	10.9	807	8 BZ506544	BZ506544 BONY446TF
35	39.4	10.9	1036	8 CC275744	CC275744 CH261-133
36	39.4	10.9	1078	5 BX461567	BX461567 BX461567
37	39	10.8	597	8 AZ471742	AZ471742 IM0286J12
38	39	10.8	919	9 CNS005RL	AL061409 Drosophila
39	39	10.8	988	8 AZ682002	AZ682002 ENTIL94TR
40	39	10.8	1092	9 CNS00DFD	AL069947 Drosophila
41	39	10.8	1633	8 BH770704	BH770704 LLMGtag45
42	38.8	10.8	592	4 BI775775	BI775775 468477 MA
43	38.8	10.8	599	6 CB460457	CB460457 720343 MA
44	38.8	10.8	612	7 CK774266	CK774266 963009 MA
45	38.8	10.8	722	9 AG298081	AG298081 Mus muscu

ALIGNMENTS

RESULT 1
T36997

LOCUS T36997 323 bp mRNA linear EST 11-JAN-1995
DEFINITION T36997 S. cerevisiae strain X2180-1A Saccharomyces cerevisiae
CDNA 3' end, mRNA sequence.
ACCESSION T36997
VERSION T36997.1 GI:620814
KEYWORDS EST.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
REFERENCE 1 (bases 1 to 323)
AUTHORS Weinstein, K.
TITLE Saccharomyces cerevisiae cDNAs
JOURNAL Unpublished (1995)
COMMENT Other ESTs: TC473
Contact: Weinstein, K. and Venter, J. C.
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org
For clone availability please contact the TIGR Database
(tdbinfo@db.tigr.org)
Seq primer: M13-21.
Location/Qualifiers
1..323
/organism="Saccharomyces cerevisiae"
/mol_type="mRNA"
/strain="X2180-1A"
/db_xref="taxon:4932"
/clone_lib="S. cerevisiae strain X2180-1A"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

FEATURES
source

ORIGIN

Query Match 17.1%; Score 61.4; DB 7; Length 323;
Best Local Similarity 61.7%; Pred. No. 0.00015;
Matches 95; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 207 AAAATCAATATAAAAAAATAAACAATCACTGATGTTTCACTAAACTCTTTAAACGC 266
AL416517 T7 end of
DB 74 AAAAATAATAAATAAAGGTAATGAATCAGCGTTCCGCACTATTTCTTTAATCTG 133
AL251956 Tetradon
QY 267 TCAACCTCAGCTTCCAACTCGCTTTGCAAAATCAGTAACACTCTCAACTTTGTCTTCCAGT 326
AL068053 Drosophila
AL097453 Drosophila

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 13, 2004, 16:30:37 ; Search time 42 Seconds
(without alignments)

4099.763 Million cell updates/sec

Title: US-09-864-486A-2

Perfect score: 402
Sequence: 1 gtaataggagtcttaagta.....aaaaaaacttaacatcact 240

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 4004546

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-O=/cgn2.1/USPTO.spool/US09864486/runat.13122004.100258.1951/app.query.fasta_1.910
-DB=A_Geneseq_23Sep04 -QWTF=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPECL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFTW=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09864486 @CGN 1.1.156 @runat.13122004.100258.1951 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	81	20.0	2185	2 AAR12141	Aar12141 Enterovir
C 2	67.5	16.6	2206	2 AAR22210	Aar22210 True type
C 3	66.5	16.4	2209	1 AAP20037	Aap20037 Sequence
C 4	66	16.3	157	6 ADA34042	Ada34042 Acinetoba
5	65	16.2	564	4 ABB66319	Abb66319 Drosophil
6	65	16.2	576	3 AAG39442	Aag39442 Arabidops
7	65	16.2	670	3 AAG39441	Aag39441 Arabidops
8	64.5	16.0	54	4 ABG08201	Abg08201 Novel hum
C 9	64.5	15.9	1140	2 AAR72386	Aar72386 XAP-1, pa
C 10	64.5	15.9	1140	4 AAU069747	Aau069747 Human xer

C 11	64.5	15.9	1140	5 ABG311550	Abg311550 Human dam
C 12	64.5	15.9	1140	5 ABB78348	Abb78348 Amino aci
C 13	64.5	15.9	1140	8 ADJ66572	Adj66572 UV-damage
C 14	64	15.8	593	2 AAY36891	Aay36891 C. tracho
15	64	15.9	618	2 AAG67089	Aag67089 Shiitake
16	64	15.9	627	2 AAW62553	Aaw62553 Protein o
17	64	15.9	627	2 AAW62552	Aaw62552 Shiitake
18	64	15.9	653	2 AAW14264	Aaw14264 Z. japoni
C 19	63	15.5	405	3 AAG09410	Aag09410 Arabidops
C 20	63	15.5	411	3 AAG09409	Aag09409 Arabidops
21	63	15.7	658	2 AAW14263	Aaw14263 S. anglic
C 22	62.5	15.4	329	5 ABB53713	Abb53713 Lactococc
C 23	62.5	15.4	1568	8 ADO42011	Ado42011 Human cel
24	62	15.4	471	6 ABU28669	Abu28669 Protein e
25	62	15.4	1689	4 ABG16013	Abg16013 Novel hum
26	62	15.4	2417	4 ABG28727	Abg28727 Novel hum
27	61.5	15.3	403	4 AAU29734	Aau29734 Novel hum
C 28	61	15.0	408	8 ADK16139	Adk16139 Nanaarcha
29	61	15.2	649	3 AAG36263	Aag36263 Arabidops
30	61	15.2	671	3 AAG36262	Aag36262 Arabidops
31	61	15.2	671	5 ABB93280	Abb93280 Herbicida
32	61	15.2	671	6 ABR39578	Abf39578 A. thalia
33	61	15.2	671	7 ADF28852	Adf28852 A. thalia
C 34	60.5	14.9	208	4 AAM16746	Aam16746 Peptide #
C 35	60.5	14.9	208	4 ABB35732	Abb35732 Peptide #
C 36	60.5	14.9	208	4 AAM29234	Aam29234 Peptide #
C 37	60.5	14.9	208	4 ABB30567	Abb30567 Peptide #
C 38	60.5	14.9	208	4 ABB21158	Abb21158 Protein #
C 39	60.5	14.9	208	4 AAM68923	Aam68923 Human bon
C 40	60.5	14.9	208	4 AAM56541	Aam56541 Human bra
C 41	60.5	14.9	208	4 ABG50588	Abg50588 Human liv
C 42	60.5	14.9	208	4 AAM04463	Aam04463 Peptide #
C 43	60.5	14.9	208	5 ABG38504	Abg38504 Human pep
C 44	60	14.9	420	3 AAY69561	Aay69561 Trametes
45	60	14.9	420	3 AAB20518	Aab20518 Trametes

ALIGNMENTS

RESULT 1

AAR12141
ID AAR12141 standard; protein; 2185 AA.
XX

AC AAR12141;

DT 25-MAR-2003 (revised)

DT 05-AUG-1991 (first entry)

XX Enteroviral polypeptide.

DE Enteroviral polypeptide.

XX Enteroviruses; monoclonal antibodies; myocarditis; myositis; meningitis;

KW encephalitis; pancreatitis; post viral fatigue.

XX Enterovirus sp.

OS Enterovirus sp.

XX DE3939200-A.

XX 29-MAY-1991.

XX 27-NOV-1989; 89DE-03939200.

XX 27-NOV-1989; 89DE-03939200.

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX Kandolf R;

XX WPI; 1991-165150/23.

XX N-PSDB; AAQ11816.

XX New enteroviral polypeptide for raising group specific antibodies - for

PT detecting any type of enterovirus in blood or serum, also new DNA

PT encoding it.

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: December 13, 2004, 17:52:37 ; Search time 11.6 Seconds

(without alignments)

2744.193 Million cell updates/sec

Title: US-09-864-486A-2

Perfect score: 402

Sequence: 1 gtaatggggttcctaagta.....aaaaaaacttaacatcact 240

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 956278

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL-frame+ n2p.model -DEV=xlh

-Q=/cgn2_1/USPTO.spool/US09864486/runat_13122004_100300_1979/app_query.fasta_1.910

-DB=Issued Patents AA -OFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0

-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi

-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15

-MODE=LOCAL -OUTPMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US09864486 @CNC 1.1.35 @runat_13122004_100300_1979 -NCPU=6 -ICPU=3

-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG

-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA.*

1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*

6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
C 1	67.5	16.6	2206	1	US-07-852-260-2
C 2	67.5	16.6	2206	2	US-08-461-503-2
C 3	67.5	16.6	2206	3	US-08-465-250-2
C 4	66	16.3	157	4	US-09-328-352-5329
C 5	65	16.2	504	4	US-09-270-767-46764
C 6	65	16.2	542	4	US-09-270-767-42841
C 7	64.5	15.9	1140	3	US-09-651-656-21
C 8	64.5	15.9	1140	3	US-09-650-855-21
C 9	61	15.0	91	4	US-09-248-796A-27715
C 10	60	14.9	410	4	US-09-684-855-143
C 11	60	14.9	420	4	US-09-684-855-120
C 12	60	14.9	420	4	US-09-488-265B-19

13	60	14.9	443	3	US-08-993-359-30	Sequence 30, Appl
14	60	14.9	443	4	US-09-273-871A-5	Sequence 5, Appli
15	60	14.9	443	4	US-09-482-558A-30	Sequence 30, Appl
16	60	14.9	443	4	US-10-083-452-5	Sequence 5, Appli
C 17	59.5	14.7	828	4	US-09-540-236-3107	Sequence 3107, Ap
C 18	59	14.7	828	4	US-09-489-039A-8129	Sequence 8129, Ap
C 19	59	14.5	547	4	US-09-555-000-2	Sequence 2, Appli
C 20	58.5	14.4	859	4	US-09-978-522-3	Sequence 3, Appli
C 21	58	14.3	328	4	US-09-248-796A-20603	Sequence 20603, A
C 22	58	14.3	442	4	US-09-684-855-137	Sequence 137, App
C 23	57.5	14.3	715	4	US-09-328-352-5229	Sequence 5229, App
C 24	57	14.2	191	4	US-09-248-796A-16718	Sequence 16718, A
C 25	57	14.0	216	4	US-09-270-767-45610	Sequence 45610, A
C 26	57	14.0	224	4	US-09-248-796A-20864	Sequence 20864, A
C 27	56.5	14.1	376	3	US-09-387-418A-13	Sequence 13, Appl
C 28	56.5	14.1	582	4	US-09-430-808A-3	Sequence 3, Appli
C 29	56.5	13.9	643	4	US-09-270-767-40779	Sequence 40779, A
C 30	56.5	13.9	643	4	US-09-270-767-55995	Sequence 55995, A
C 31	56.5	14.1	712	1	US-08-369-796-6	Sequence 6, Appli
C 32	56.5	14.1	712	2	US-08-852-091-6	Sequence 6, Appli
C 33	56.5	14.1	712	2	US-08-820-754-6	Sequence 6, Appli
C 34	56.5	14.1	712	3	US-08-956-652-6	Sequence 6, Appli
C 35	56.5	14.1	712	3	US-08-956-869-6	Sequence 6, Appli
C 36	56.5	14.1	712	3	US-08-948-547-6	Sequence 6, Appli
C 37	56.5	14.1	712	3	US-08-956-653A-6	Sequence 6, Appli
C 38	56.5	14.1	712	4	US-08-212-185-6	Sequence 6, Appli
C 39	56.5	14.1	712	4	US-09-430-808A-2	Sequence 2, Appli
C 40	56.5	14.1	712	5	PCT-US95-17025-6	Sequence 6, Appli
C 41	56.5	14.1	729	4	US-09-917-254-97	Sequence 97, Appl
C 42	56.5	14.1	740	1	US-08-276-099A-12	Sequence 12, Appl
C 43	56.5	14.1	740	1	US-08-781-890-12	Sequence 12, Appl
C 44	56.5	14.1	750	1	US-08-369-796-4	Sequence 4, Appli
C 45	56.5	14.1	750	2	US-08-852-091-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-07-852-260-2

; Sequence 2, Application US/078522260

; Patent No. 5525715

; GENERAL INFORMATION:

; APPLICANT: Racanelli, Vincent

; APPLICANT: Tatem, Joanne M.

; APPLICANT: Weeks-Levy, Carolyn L.

; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS: CDNA

; ADDRESSER: Cooper & Dunham

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/852,260

; FILING DATE: 19920619

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 36607-B-PCT-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 977-9550

; TELEFAX: (212) 664-0525

; TELEX: 422523 COOP UI

; INFORMATION FOR SEQ ID NO: 2:

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 13, 2004, 18:14:18 ; Search time 37.2 Seconds
(without alignments)
4608.753 Million cell updates/sec

Title: US-09-864-486A-2
Perfect score: 402
Sequence: 1 gcaataggagtcttaagta.....aaaaaaacttaacatcact 240

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1585576 seqs, 357178320 residues
Total number of hits satisfying chosen parameters: 3171152

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result * Query

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2	70	17.4	386	17	US-10-425-115-194870	Sequence 194870, A
3	69.5	17.1	157	15	US-10-424-599-236702	Sequence 236702, A
4	69	17.0	187	15	US-10-425-114-44299	Sequence 44299, A
5	67.5	16.6	148	15	US-10-424-599-150125	Sequence 150125, A
6	67.5	16.6	154	17	US-10-425-115-218584	Sequence 218584, A
7	67	16.5	89	15	US-10-424-599-242199	Sequence 242199, A
8	67	16.7	663	16	US-10-437-963-188657	Sequence 188657, A
9	64.5	15.9	89	17	US-10-425-115-297092	Sequence 297092, A
10	64.5	15.9	1140	16	US-10-468-406-8	Sequence 8, Appli
11	64	15.8	325	15	US-10-424-599-254766	Sequence 254766, A
12	63	15.5	413	15	US-10-425-114-39092	Sequence 39092, A
13	62.5	15.4	112	17	US-10-425-115-222873	Sequence 222873, A
14	62.5	15.4	329	14	US-10-369-493-18334	Sequence 18334, A
15	62	15.4	104	15	US-10-424-599-169421	Sequence 169421, A
16	62	15.3	231	15	US-10-424-599-273714	Sequence 273714, A
17	62	15.4	471	15	US-10-282-122A-56593	Sequence 56593, A
18	62	15.4	636	16	US-10-437-963-184530	Sequence 184530, A
19	61	15.0	108	15	US-10-424-599-179712	Sequence 179712, A
20	61	15.2	671	14	US-10-217-939-14	Sequence 14, Appl
21	60.5	14.9	120	15	US-10-425-114-43581	Sequence 43581, A
22	60.5	14.9	208	9	US-09-864-761-36456	Sequence 36456, A
23	60	14.9	410	14	US-10-442-538-143	Sequence 143, App
24	60	14.9	420	14	US-10-442-538-120	Sequence 120, App
25	60	14.9	443	10	US-09-999-214-30	Sequence 30, Appl
26	60	14.9	443	13	US-10-083-452-5	Sequence 5, Appli
27	60	14.9	443	16	US-10-734-510-5	Sequence 5, Appli
28	60	14.9	962	16	US-10-437-963-187589	Sequence 187589, A
29	59.5	14.7	73	15	US-10-424-599-185823	Sequence 185823, A
30	59.5	14.7	85	15	US-10-424-599-188894	Sequence 188894, A
31	59.5	14.7	120	15	US-10-424-599-212424	Sequence 212424, A
32	59.5	14.7	737	15	US-10-425-114-57283	Sequence 57283, A
33	59.5	14.7	747	15	US-10-282-122A-63122	Sequence 63122, A
34	59	14.5	174	15	US-10-406-686A-53	Sequence 53, Appl
35	59	14.7	218	14	US-10-389-493-2768	Sequence 2768, Ap
36	59	14.7	472	15	US-10-282-122A-59548	Sequence 59548, A
37	58.5	14.6	207	15	US-10-264-049-2701	Sequence 2701, Ap
38	58.5	14.6	225	15	US-10-424-599-177258	Sequence 177258, A
39	58.5	14.4	859	10	US-09-978-522-3	Sequence 3, Appli
40	58	14.3	63	16	US-10-437-963-142126	Sequence 142126, A
41	58	14.4	391	15	US-10-282-122A-55899	Sequence 55899, A
42	58	14.4	400	14	US-10-369-493-1129	Sequence 1129, Ap
43	58	14.4	442	14	US-10-442-538-137	Sequence 137, App
44	58	14.4	450	15	US-10-282-122A-43729	Sequence 43729, A
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ALIGNMENTS

RESULT 1
US-10-767-701-49593
; Sequence 49593, Application US/10767701
; Publication NO. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 49593
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3476-061-P1-K1-B10.pbp
US-10-767-701-49593

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: December 13, 2004, 17:56:18 ; Search time 12 Seconds

(without alignments)
3848.671 Million cell updates/sec

Title: US-09-864-486A-2

Perfect score: 402

Sequence: 1 gtaataggagtcttaagta.....aaaaaaacttaacatcact 240

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	88	21.7	2201	1	genome polyprotein
C 2	81	20.0	2185	1	genome polyprotein
C 3	81	20.0	2185	1	genome polyprotein
C 4	67.5	16.8	401	2	probable aminotran
C 5	67.5	16.6	2206	1	genome polyprotein
C 6	67.5	16.6	2206	2	genome polyprotein
C 7	66.5	16.4	2206	1	genome polyprotein
C 8	66.5	16.4	2207	1	genome polyprotein
C 9	66.5	16.4	2209	1	genome polyprotein
C 10	66.5	16.4	2209	1	genome polyprotein
C 11	66	16.3	1379	2	genome polyprotein
C 12	65	16.2	628	2	phosphoenolpyruv
C 13	64.5	15.9	1140	1	UV-damaged DNA-bin
C 14	64.5	15.9	1140	1	UV-damaged DNA-bin

C 15	64.5	15.9	1140	2	JC7152
C 16	64	15.9	355	2	F96940
C 17	64	15.8	593	2	A71532
C 18	64	15.9	670	2	S52637
C 19	64	15.8	2182	1	GNNYB1
C 20	63	15.5	405	2	T45615
C 21	62.5	15.4	329	2	F86675
C 22	62.5	15.4	2214	1	A48548
C 23	62	15.4	471	2	D64973
C 24	62	15.4	471	2	F90988
C 25	62	15.4	471	2	H85833
C 26	62	15.4	634	2	A32241
C 27	62	15.3	2185	1	JQ2021
C 28	61	15.0	292	2	AG2225
C 29	61	15.2	671	2	T06034
C 30	61	15.0	2185	1	GNNYSV
C 31	61	15.0	2185	1	GNNYSH
C 32	60.5	14.9	1611	2	T38236
C 33	60.5	14.9	2207	2	S09553
C 34	60	14.8	298	2	B71685
C 35	59.5	14.8	406	2	A10292
C 36	59.5	14.7	2206	1	GNNY21
C 37	59	14.7	218	2	S76407
C 38	59	14.5	547	2	F69964
C 39	58	14.3	76	2	T42153
C 40	58	14.3	396	2	D97133
C 41	58	14.3	400	1	F69142
C 42	58	14.4	450	2	AB0771
C 43	58	14.3	5762	2	A41819
C 44	57.5	14.3	483	2	A25896
C 45	57.5	14.2	576	2	S12792

ALIGNMENTS

RESULT 1

GNNYA9
Genome polyprotein - coxsackievirus A9 (strain Griggs)
N:Contains: coat protein 1A; coat protein 1B; coat protein 1C; coat protein 1D; core p
polymerase (EC 2.7.7.48)
C:Species: coxsackievirus A9
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: JQ0523
J.Chang, K.H.; Auvinen, P.; Hyypia, T.; Stanway, G.
J. Gen. Virol. 70, 3269-3280, 1989
A:Title: The nucleotide sequence of coxsackievirus A9: implications for receptor bindi
A:Reference number: JQ0523; MUID:90111704; PMID:2558158
A:Accession: JQ0523
A:Molecule type: mRNA
A:Residues: 1-2201 <CHA>
A:Cross-references: UNIPROT:P21404
C:Superfamily: poliovirus genome polyprotein
C:Keywords: coat protein; core protein; genome-linked protein; nucleotidyltransferase;
F:1-69/Product: coat protein 1A #status predicted <VP4>
F:70-330/Product: coat protein 1B #status predicted <VP2>
F:331-568/Product: coat protein 1C #status predicted <VP3>
F:569-870/Product: coat protein 1D #status predicted <VP1>
F:871-1017/Product: core protein 2A #status predicted <2AP>
F:1018-1116/Product: core protein 2B #status predicted <2BP>
F:1117-1145/Product: core protein 2C #status predicted <2CP>
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F:1535-1556/Product: genome-linked protein VPg #status predicted <VPG>
F:1557-1739/Product: proteinase #status predicted <PTS>
F:1740-2201/Product: RNA-directed RNA polymerase #status predicted <RPS>
F:1537/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

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Length: 2201
Matches: 20
Conservative: 15
Mismatch: 23
Indels: 6
Gaps: 2

Qy 233 TTAAGTTTTTTTATATATGATTTTGAAATTGAAAAATTTTATCCAAAGTCGTTTGTAGTA 174

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2004, 14:03:27 ; Search time 1385.6 Seconds
(without alignments)
8191.056 Million cell updates/sec

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Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
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9: gb_pr.*
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11: gb_srs.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	240	100.0	360	6	AX323247 Sequence
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4	44	18.3	99202	10	AL928807 Mouse DNA
5	41	17.1	136268	10	AC068496
6	41	17.1	213482	10	AC073883
7	40.8	17.0	132728	2	AC099411
8	40.6	16.9	198973	2	CR628332
9	39.6	16.5	244962	2	AC098272
10	39.6	16.5	251257	2	AC095972
11	39.2	16.3	128277	2	AC099410
12	38.2	15.9	12763	6	AX345204
13	38.2	15.9	103507	5	AL928618
14	38.2	15.9	110000	2	AY657029 ¹
15	38.2	15.9	150663	2	AC074258
16	38.2	15.9	184431	10	AC130822
17	38.2	15.9	211697	10	AC122296
18	38	15.8	170559	2	AC026989
19	38	15.8	182997	9	AL355332

c	20	37.8	15.8	97621	9	AL607089	Human DNA
c	21	37.8	15.8	349980	6	AX344560	Sequence
c	22	37.6	15.7	9238	6	AX323752	Sequence
c	23	37.6	15.7	121922	2	AP000576	Homo sapi
c	24	37.6	15.7	233181	2	AC111558	Rattus no
c	25	37.4	15.6	180137	2	EX957257	Danio rer
c	26	37.2	15.5	281723	3	PFA929359	Plasmodiu
c	27	37	15.4	72000	9	AP003386	AP003386 Homo sapi
c	28	37	15.4	162397	2	AC011098	Homo sapi
c	29	37	15.4	169993	2	AC144884	Papio anu
c	30	37	15.4	210223	10	AC122183	Mus muscu
c	31	37	15.4	210567	2	AC074215	Homo sapi
c	32	37	15.4	216031	9	AC011328	Homo sapi
c	33	37	15.4	234203	2	AC121311	Mus muscu
c	34	36.8	15.3	59623	9	AC020591	AC020591 Homo sapi
c	35	36.8	15.3	110000	2	EX005127 ²	Continuation (3 of
c	36	36.8	15.3	110000	2	EX005127 ³	Continuation (4 of
c	37	36.8	15.3	177070	2	AC018875	Homo sapi
c	38	36.8	15.3	201823	9	HSG120K12	AL109865 Human DNA
c	39	36.8	15.3	204483	10	AL671990	AL671990 Mouse DNA
c	40	36.6	15.2	18683	6	AX281292	Sequence
c	41	36.6	15.2	18683	6	AX345215	Sequence
c	42	36.4	15.2	4895	14	AF156933	AF156933 Hyposoter
c	43	36.4	15.2	54814	4	AC104718	Sus scrof
c	44	36.4	15.2	107893	5	EX276180	Zebrafish
c	45	36.4	15.2	146776	2	EX897667	Danio rer

ALIGNMENTS

RESULT 1
BD175189
LOCUS BD175189
DEFINITION DNA fragment of a mechiru nutrition nature picha pathtorisu yeast
ACCESSION BD175189
VERSION BD175189.1 GI:29120883
KEYWORDS JP 2002253235-A/2.
SOURCE Pichia pastoris
ORGANISM Pichia pastoris
REFERENCE Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetaceae; Pichia.
AUTHORS Dias,J.M., Prado,I.V. and Leon,N.C.
TITLE DNA fragment of a mechiru nutrition nature picha pathtorisu yeast
JOURNAL ICL gene
COMMENT Patent: JP 2002253235-A 2 10-SEP-2002;
CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA
OS Pichia pastoris (yeast)
PN JP 2002253235-A/2
PD 10-SEP-2002
PF 28-MAY-2000 JP 2001159321
PI JAVIER MENENDEZ DIAS,IRIS VALDEZ PRADO,NELSON CABRERA LEON PC
C12N15/09,C12N15/00
CC Secuencia que contiene la region 3' no codificante del gen CC
FH Key Location/Qualifiers
FT terminator Location/Qualifiers
1..360
/organism="Pichia pastoris"
/mol_type="genomic DNA"
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Best Local Similarity 100.0%; Pred. No. 2.4e-52;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QV 1 GTAATAGGAGTTCCTAAGTAGTTAAGATAATTCAGCTTGAGCTATTATAGATTGTGTGT 60
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2004, 14:02:37 ; Search time 226 Seconds
(without alignments)
5574.606 Million cell updates/sec

Title: US-09-864-486A-2
Perfect score: 240
Sequence: 1 gtaataggagttcctaagta.....aaaaaaaaaacttaacatcaact 240

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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- 12: _geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	38.2	15.9	12763	ABL32302	Human imm
3	37.6	15.7	9238	ABK28366	DNA trans
4	37	15.4	5155	ABN87364	Human lip
5	36.8	15.3	32186	AAS34422	Human DNA
6	36.8	15.3	38855	ADN41808	Novel hum
7	36.6	15.2	18683	ABL32313	Human imm
8	36.6	15.2	18683	ABL32313	Human imm
9	36	15.0	6127	ABL54334	Chemical
10	36	15.0	6127	ABL34449	Human met
11	36	15.0	9919	ABL70120	Chemical
12	36	15.0	9919	AAV04631	A. thalia
13	35.8	14.9	6123	ABL32821	Arabidops
14	35.8	14.9	6509	ABL32226	Human imm
15	35.2	14.7	7276	ABL32903	Human imm
16	35	14.6	4570	ABL29394	Human imm
17	35	14.6	6987	ABL29562	Drosophil
18	34.8	14.5	5814	ABL32974	Human imm
19	34.6	14.4	16688	ABL32320	Human imm
20	34.2	14.3	5942	ABZ10233	Haematopo
21	34.2	14.3	5942	ABZ10147	Haematopo

C	22	34.2	14.3	5942	10	ADE84143
	23	34.2	14.3	15161	6	ABL70458
	24	34.2	14.3	15161	6	AAS61423
C	25	34.2	14.3	15872	4	AAS46520
	26	34	14.2	1900	3	AAF15888
C	27	34	14.2	6360	6	ABL34398
	28	33.8	14.1	606	5	ABV49913
	29	33.8	14.1	7833	10	ADB54184
C	30	33.8	14.1	7833	10	ADB54312
C	31	33.8	14.1	7833	10	ADE37769
C	32	33.8	14.1	7833	10	ADE37779
C	33	33.8	14.1	8718	6	ABL33273
	34	33.6	14.0	799	4	AH31386
	35	33.6	14.0	1325	6	ABZ21184
C	36	33.6	14.0	16766	6	ABL33864
C	37	33.6	14.0	16766	6	ABL34157
	38	33.6	14.0	110000	5	AAF84800
C	39	33.4	13.9	6963	6	ABL32978
C	40	33.4	13.9	14798	6	ABL33032
C	41	33.4	13.9	15121	6	ABN80239
C	42	33.4	13.9	17137	6	ABL32191
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C	45	33.2	13.8	110000	3	AAF22305_01

ALIGNMENTS

RESULT 1

ABK13231

ID ABK13231 standard; DNA; 360 BP.

XX AC ABK13231;

XX AC ABK13231;

DT 23-APR-2002 (first entry)

XX P. pastoris isocitrate lyase gene 3' UTR.

DE Isocitrate lyase; ICL; 3' UTR; ds; yeast; heterologous gene expression.

KW Isocitrate lyase; ICL; 3' UTR; ds; yeast; heterologous gene expression.

XX Pichia pastoris.

XX EP1162266-A2.

XX PD 12-DEC-2001.

XX PF 28-MAY-2001; 2001EP-00202009.

XX PR 26-MAY-2000; 2000CU-00000122.

XX (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.

XX Menendez Diaz J, Valdes Prado I, Cabrera Leon N;

XX WPI; 2002-084415/12.

XX New recombinant DNA fragment for protein production, contains an

XX isocitrate lyase encoding gene from Pichia pastoris, which regulates

XX heterologous gene expression in yeasts, when operably linked to the

XX fragment.

XX Claim 1; Page 8; 18pp; English.

XX The invention relates to a recombinant DNA fragment (I) comprising a

XX sequence (S) of 68bp (the 5' region of the Pichia pastoris isocitrate

XX lyase, ICL, gene including the promoter) or 360bp (the 3' UTR including a

XX terminator), given in the specification, where (I) belongs to an

XX isocitrate lyase encoding gene (ICL) from Pichia pastoris, which is able

XX to regulate heterologous gene expression in yeasts, when it is operably

XX linked to (I), and including regulatory elements necessary for

XX heterologous gene expression. The DNA fragment is useful for expressing

XX heterologous proteins in Pichia pastoris, for expressing a foreign gene,

XX

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2004, 14:11:07 ; Search time 45.2 Seconds
(without alignments)
3774.100 Million cell updates/sec

Title: US-09-864-486A-2
Perfect score: 240
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Scoring table: IDENTITY_NUC
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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	32.6	13.6	65933	4	US-09-543-771-11
C 5	32	13.3	11049	4	US-10-204-708-22
C 6	31.6	13.2	6306	4	US-10-204-708-50
C 7	31.4	13.1	1347	3	US-09-134-001C-218
C 8	31.4	13.1	1347	4	US-09-710-279-1727
C 9	31.4	13.1	4069	4	US-09-710-279-3976
C 10	31.2	13.0	164	4	US-09-621-976-16692
C 11	31.2	13.0	669	4	US-09-799-451-750
C 12	31.2	13.0	2169	3	US-08-981-803-14
C 13	31.2	13.0	2169	3	US-08-981-803-28
C 14	31.2	13.0	2169	3	US-08-983-440-14
C 15	31.2	13.0	2169	3	US-08-983-440-28
C 16	31.2	13.0	2169	4	US-09-367-895-14
C 17	31.2	13.0	2169	4	US-09-367-895-28
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C 19	31.2	13.0	11469	4	US-09-367-895-29
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C 21	31.2	13.0	11478	3	US-08-983-440-29
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C 24	30.8	12.8	458	4	US-09-270-767-3713
C 25	30.8	12.8	791	3	US-08-998-416-346
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C 28	30.6	12.8	5501	4	US-10-204-708-37	Sequence 37, Appl
C 29	30.6	12.8	11049	4	US-10-204-708-21	Sequence 21, Appl
C 30	30.6	12.8	11049	4	US-10-204-708-21	Sequence 21, Appl
C 31	30.4	12.7	516	4	US-08-956-171E-597	Sequence 597, App
C 32	30.4	12.7	516	4	US-08-781-986A-597	Sequence 597, App
C 33	30.4	12.7	11050	4	US-10-204-708-86	Sequence 86, Appl
C 34	30.4	12.7	11811	3	US-09-078-294-7	Sequence 7, Appl
C 35	30.4	12.7	19513	4	US-10-204-708-39	Sequence 39, Appl
C 36	30.2	12.6	972	1	US-07-915-934-1	Sequence 1, Appl
C 37	30.2	12.6	972	1	US-08-325-743-1	Sequence 1, Appl
C 38	30.2	12.6	1674	4	US-09-248-796A-10284	Sequence 10284, A
C 39	30.2	12.6	1722	4	US-09-248-796A-6457	Sequence 6457, A
C 40	30.2	12.6	5666	4	US-10-204-708-29	Sequence 29, Appl
C 41	30.2	12.6	6866	4	US-10-204-708-20	Sequence 20, Appl
C 42	30.2	12.6	193303	4	US-09-497-855A-37	Sequence 37, Appl
C 43	30.2	12.6	193303	4	US-09-497-855A-44	Sequence 44, Appl
C 44	30	12.5	8578	4	US-09-784-358-17	Sequence 17, Appl
C 45	29.8	12.4	516	4	US-09-601-198-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/08880179
; Patent No. 6091004
; GENERAL INFORMATION:
; APPLICANT: Ryals, John
; APPLICANT: Delaney, Terry
; APPLICANT: Friedrich, Leslie
; APPLICANT: Weymann, Kristianna
; APPLICANT: Lawton, Kay
; APPLICANT: Ellis, Daniel
; APPLICANT: Uknes, Scott
; APPLICANT: Jesse, Taco
; APPLICANT: Vos, Pieter
; TITLE OF INVENTION: GENE ENCODING A PROTEIN INVOLVED IN THE
; TITLE OF INVENTION: SIGNAL TRANSDUCTION CASCADE LEADING TO SYSTEMIC ACQUIRED RES
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6091004artis Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,179
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Weigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1909
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9919 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

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5606.970 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 8171462

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SUMMARIES

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c 5	37.6	15.7	9238	15	US-10-240-453-240
6	37	15.4	55155	9	US-09-735-933-3
c 7	36.8	15.3	38855	11	US-09-973-278-936
c 8	36.2	15.2	18683	15	US-10-311-455-286
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c 10	36	15.0	6127	15	US-10-240-485-2
c 11	36	15.0	9919	13	US-10-079-035-1
12	35.8	14.9	2829	18	US-10-425-115-172689

c 13	35.8	14.9	6123	15	US-10-311-455-794	Sequence 794, App
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c 15	35.4	14.8	3673778	15	US-10-312-841-2	Sequence 2, Appli
c 16	35.2	14.7	7276	15	US-10-311-455-876	Sequence 876, App
c 17	35.2	14.7	3673778	15	US-10-312-841-1	Sequence 1, Appli
c 18	34.8	14.5	637	13	US-10-027-632-201748	Sequence 201748,
c 19	34.8	14.5	637	13	US-10-027-632-201749	Sequence 201749,
c 20	34.8	14.5	637	15	US-10-027-632-201748	Sequence 201748,
c 21	34.8	14.5	637	15	US-10-027-632-201749	Sequence 201749,
c 22	34.8	14.5	5814	15	US-10-311-455-947	Sequence 947, App
c 23	34.6	14.4	16688	15	US-10-311-455-293	Sequence 293, App
c 24	34.4	14.3	590	13	US-10-027-632-227310	Sequence 227310,
c 25	34.4	14.3	590	13	US-10-027-632-227311	Sequence 227311,
c 26	34.4	14.3	590	13	US-10-027-632-227312	Sequence 227312,
c 27	34.4	14.3	590	15	US-10-027-632-227310	Sequence 227310,
c 28	34.4	14.3	590	15	US-10-027-632-227311	Sequence 227311,
c 29	34.4	14.3	590	15	US-10-027-632-227312	Sequence 227312,
c 30	34.2	14.3	382	18	US-10-425-115-74299	Sequence 74299, A
c 31	34.2	14.3	5942	18	US-10-473-126-287	Sequence 287, App
c 32	34.2	14.3	5942	18	US-10-473-126-373	Sequence 373, App
c 33	34.2	14.3	15161	16	US-10-221-613-386	Sequence 386, App
c 34	34.2	14.3	15872	16	US-10-221-714A-242	Sequence 242, App
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c 36	34	14.2	6960	15	US-10-311-455-2371	Sequence 2371, Ap
c 37	33.8	14.1	338	16	US-10-242-535A-13681	Sequence 13681, A
c 38	33.8	14.1	338	16	US-10-085-783A-13681	Sequence 13681, A
c 39	33.8	14.1	8718	15	US-10-311-455-1246	Sequence 1246, Ap
c 40	33.6	14.0	6196	15	US-10-311-455-1837	Sequence 1837, Ap
c 41	33.6	14.0	16766	15	US-10-311-455-2130	Sequence 2130, Ap
c 42	33.4	13.9	6963	15	US-10-311-455-951	Sequence 951, App
c 43	33.4	13.9	14798	15	US-10-311-455-1005	Sequence 1005, Ap
c 44	33.4	13.9	17137	15	US-10-311-455-164	Sequence 164, App
c 45	33.2	13.8	9110	16	US-10-221-714A-116	Sequence 116, App

ALIGNMENTS

RESULT 1

US-09-864-486A-2
; Sequence 2, Application US/09864486A
; Publication No. US20040106783A1
; GENERAL INFORMATION:
; APPLICANT: Menendez Diaz, Javier
; APPLICANT: Valdes Prado, Chris
; APPLICANT: Cabrera Leon, Nelson
; TITLE OF INVENTION: DNA Fragments of the Methylotrophic Pichia Pastoris Yeast iCL g
; FILE REFERENCE: 976-9
; CURRENT APPLICATION NUMBER: US/09/864,486A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Pichia pastoris
; US-09-864-486A-2

Query Match 100.0%; Score 240; DB 11; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.9e-54;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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5785.615 Million cell updates/sec

Title: US-09-864-486A-2
Perfect score: 240
Sequence: 1 gtaatagaggtcttaagta.....aaaaaaacttaacatcact 240

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gssi:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	46	19.2	476	1	AI399548 NCSPE6C2T7
C 2	39.8	16.6	329	6	CF329701 NACL--05-
C 3	38.4	16.0	519	5	BU533351 AGENCOURT
C 4	38.4	16.0	568	9	CC847190 ND.L.9714.
C 5	38.2	15.9	395	7	CO819665 CSECS157H
C 6	38.2	15.9	531	7	CF479344 RIW3_23_
C 7	38.2	15.9	757	9	AG495046 Mus muscu
C 8	38	15.8	282	5	BU564984 AGENCOURT
C 9	38	15.8	500	6	CA396793 cs82c02.y
C 10	37.8	15.8	865	9	CL130913 ISB1-98N2
C 11	37.4	15.6	1201	9	AL106036 Drosophil
C 12	37.2	15.5	168	4	BI744958 rk94d10.y
C 13	37.2	15.5	265	4	BM343692 rr41g09.y
C 14	37.2	15.5	1101	9	AL063921 Drosophil
C 15	37	15.4	127	1	AI865961 wk87g01.x
C 16	37	15.4	563	7	CN985874 61448 125
C 17	37	15.4	707	6	CF207352 CAB20001
C 18	37	15.4	870	5	BQ933590 AGENCOURT
C 19	36.8	15.3	646	5	BU485437 603468625
C 20	36.8	15.3	686	5	BU208472 604151831
C 21	36.8	15.3	733	7	CR577504 CR577504
C 22	36.8	15.3	886	9	CL134229 ISB1-104K
C 23	36.8	15.3	938	7	CK020362 AGENCOURT
C 24	36.8	15.3	1204	9	AL106628 Drosophil

25	36.8	15.3	10560	8	AQ839853
26	36.6	15.2	296	5	BQ106987 NXLV085_B
27	36.6	15.2	511	9	TA128B12Q
28	36.6	15.2	703	9	CC503344 CH240_342
29	36.6	15.2	920	9	CNS0046U
30	36.6	15.2	1101	9	CNS0024Y
31	36.4	15.2	615	2	BF299319
32	36.4	15.2	662	9	EX225916
33	36.4	15.2	1101	9	CNS00296
34	36.4	15.2	1101	9	CNS016TA
35	36.2	15.1	270	6	CB218381
36	36.2	15.1	286	7	H23747 yn70h07.sl
37	36.2	15.1	537	5	BX522361
38	36.2	15.1	585	9	CE699052 tigr-g88-
39	36.2	15.1	687	1	AL855043
40	36.2	15.1	722	4	BM690925 UI-B-C11-
41	36.2	15.1	783	3	AY067688 Schmidtea
42	36	15.0	605	2	AW307435 sf5h12.y
43	36	15.0	613	9	BX213573 Danio rer
44	35.8	14.9	481	8	BZ618173
45	35.8	14.9	486	1	AL714653

ALIGNMENTS

RESULT 1
AI399548/c
LOCUS
DEFINITION
NCSPE6C2T7 Subtracted Perithecial Neurospora crassa cDNA clone SP6C2
3', similar to ORF YLR251w, probable membrane protein, mRNA
sequence.
AI399548 476 bp mRNA linear EST 08-FEB-1999
VERSION
AI399548.1 GI:4242635
KEYWORDS
EST.
SOURCE
Neurospora crassa
ORGANISM
Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE
1 (bases 1 to 476)
Nelson,M.A., Kang,S., Braun,E.L., Crawford,M.E., Dolan,P.L.,
Leonard,P.M., Mitchell,J., Armiijo,A.M., Bean,L., Blueves,E.,
Cushing,T., Errett,A., Fleharty,M., Gorman,M., Judson,K.,
Miller,R., Ortega,J., Pavlova,I., Perea,J., Todisco,S.,
Trujillo,R., Valentine,J., Wells,A., Werner-Washburne,M., Yazzie,S.
and Natvig,D.O.
Expressed sequences from conidial, mycelial, and sexual stages of
Neurospora crassa
Fungal Genet. Biol. 21, 348-363 (1997)
JOURNAL
MEDLINE
97435349
PUBMED
9290248
COMMENT
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Castetter Hall, Albuquerque, NM 87131, USA
Tel: 505 277 3411
Fax: 505 277 0304
Email: ngp@biology.unm.edu.
Location/Qualifiers
1..476
/organism="Neurospora crassa"
/mol_type="mRNA"
/strain="fl a (FGSC 4347)"
/db_xref="taxon:5141"
/clone="SP6C2"
/sex="Mating type a (fluffy), fertilized"
/tissue_type="Perithecia"
/dev_stage="Fruiting Body"
/lab_host="E. coli"
/clone_lib="Subtracted Perithecial"
/note="Vector: pBluescript SK (-); Site 1: EcoRI; Site 2:
XhoI; mRNA isolated from 5 day old perithecia (fruiting
bodies) of the fluffy strain fl a (Mating type a),